

[illegible]

**FIG. 1**

	I	II	III	
TA01	MPSTHRAGSLKDPEIAELFPKEDPEKLTDLRETOHQSFOAVYFAKDVNRTHVEVAIKKMSYSKQSTKXW---QDI I KEV 77			
TA02	MPAGGRAGSLKDIDVAELFFKDDPEKLFSDLRETOHQSFOAVYFAKDVNRSEVVAIKKMSYSKQSTKXW---QDI I KEV 77			
CTAO	-MAPAVIUKWIKIDPSTAAIFSHKDPEDLRETOHQSFOAVYFAKDVNRSEVVAIKKMSYSKQSTKXW---NDI I KEV 76			
STE20	REERERRKKQLYAKLNEICSDGDPSTKYAHLVKIQQASGGVYTAIETGTHVSVAIKQWNLK-QPKKELIIRHILVMK 670			
	IV	V	VI	
TA01	KFLQRIKHPNSIEYKGCYLRENTAMLVMEYCLQASDLLELVKKPLQVEVEIAAITHGALQGLAYLHBIHTMIHRDIKAGN 156			
TA02	RFLQRIKHPNTIOYRGCYLRENTAMLVMEYCLQASSEFLEVIKPKPLQVEVEIAAVTIGALQGLAYLHBIHTMIHRDIKAGN 156			
CTAO	SFLNTVVRPHIIVDYKACFLKDTTCMLVMEYCIQSAADIVDLVRKGMREVEIAAICSQTLDAKRYLHBIHTMIHRDIKAGN 155			
STE20	Q-----SKRPHIVNFIDSVVLKCDLWVIMEYHEGGSUTDV-VTHICILTEGQIGAVCRETLSOLEFLH8KGVILHRDIKSDM 744			
	VII	VIII	IX	
TA01	ILLTEPGQVKLADTOSAS-----MASPANSFVOTPYWNAPEVILAMDEGOYDCKVDVMBLQITCIELAERKPPPLFNMA 230			
TA02	ILLSEFGLVKLGDPOSAS-----INAPAHISFVOTPYWNAPEVILAMDEGOYDCKVDVMBLQITCIELADRKPPPLFNMA 230			
CTAO	ILLSDHAIYVKLADTOSAS-----LVDPAQTFIOTPPFFNAPEVILAMDEGHYTDRAIDMBLQITCIELAERKPPPLFSMA 229			
STE20	ILLSHEGDIKLTDTGFCQAQINELNLKRTTMTVOTPYWNAPEVVSRLK-----XGPKVDIMBLOIMIMIEGEPPLNETP 819			
	X	XI		
TA01	MSALYHIAQNESPTLQSNWSDFRN-----FVDSCLQKIPQDRPTSE 273			
TA02	MSALYHIAQNESPALQSNHSEYFRN-----FVDSCLQKIPQDRPTSE 273			
CTAO	MSALYHIAQNDPPTLSPIDTSEQPEWSLEFVQFIDKCLRKPAEEMSAE 279			
STE20	LRLVLIATNGTKPKLPENLSS---SLKK--FLDWCLCPEPEDRASAT 863			

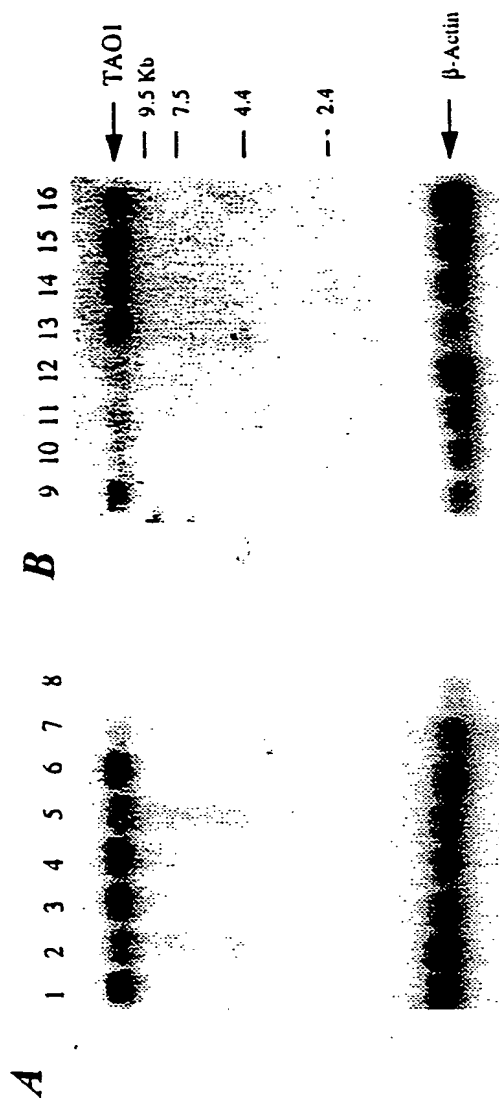
FIG. 2

**A**

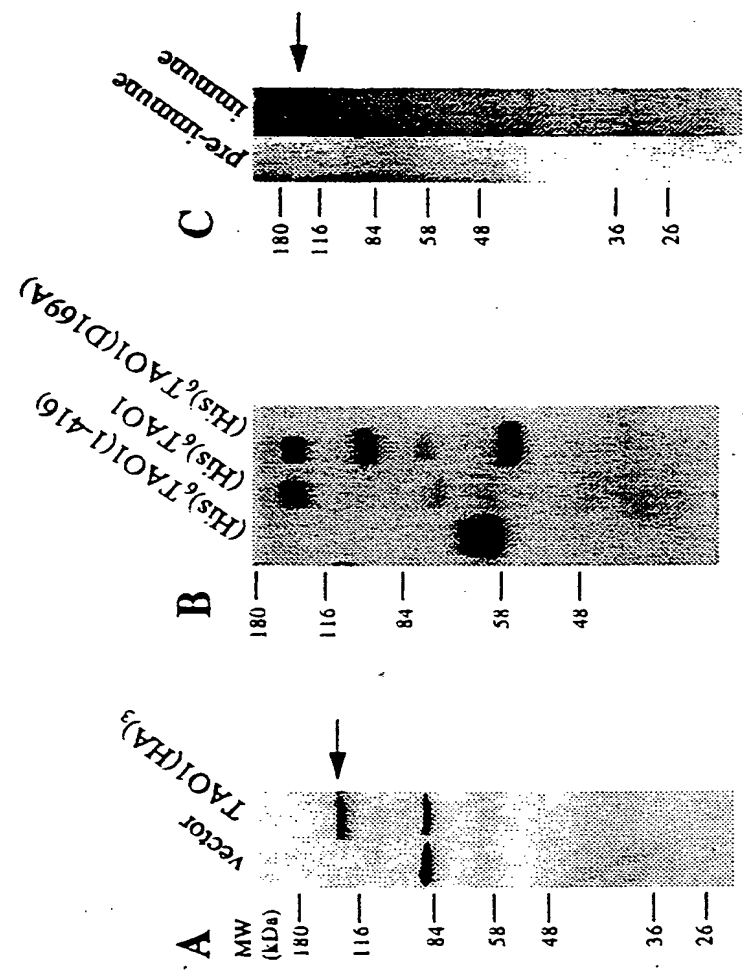
Brain    Muscle    Heart    Liver    Kidney    Lung    Testis    Epididymus    Spleen

— 9.4 Kb  
— 5.0  
— 4.2  
— 2.3  
— 2.0

**FIGS. 3A and 3B**



**FIGS. 4A and 4B**



FIGS. 5A-5C

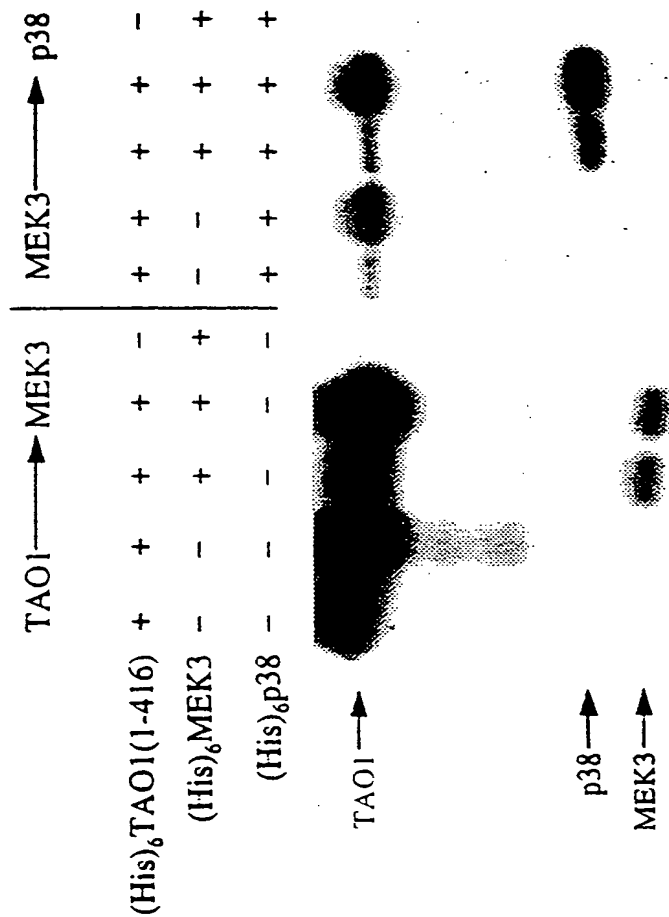


FIG. 6

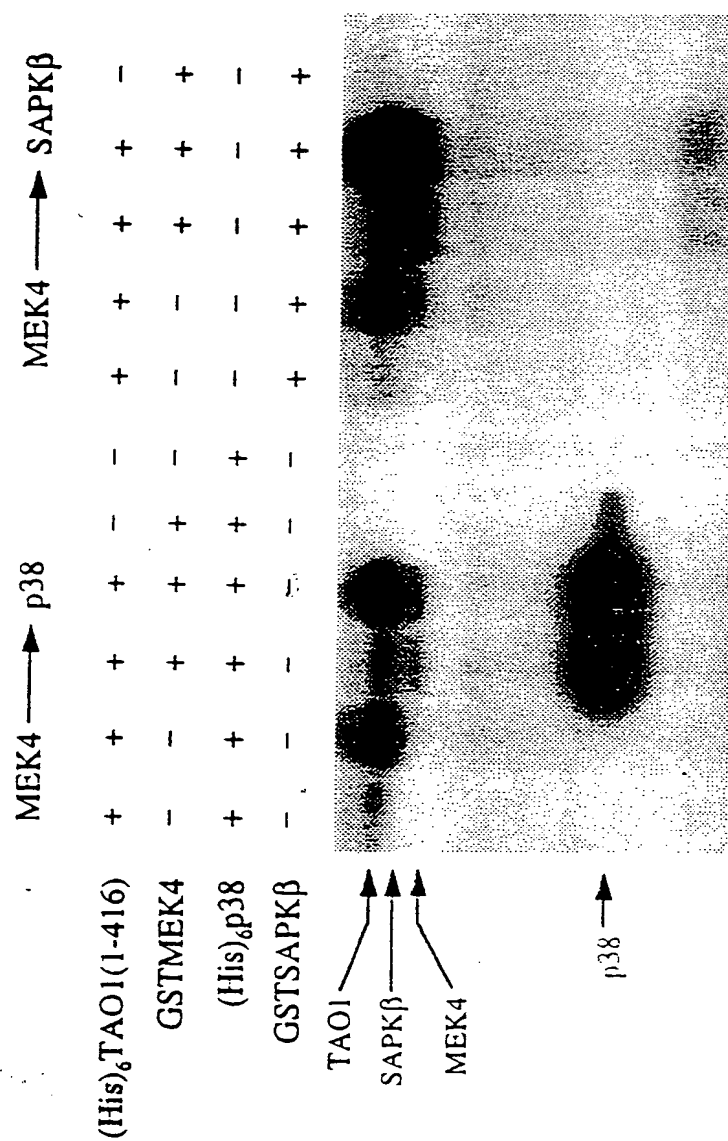


FIG. 7

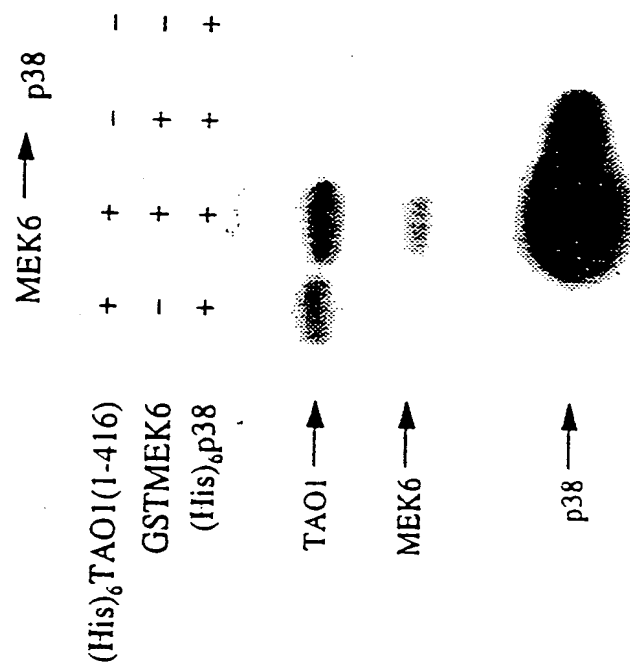


FIG. 8



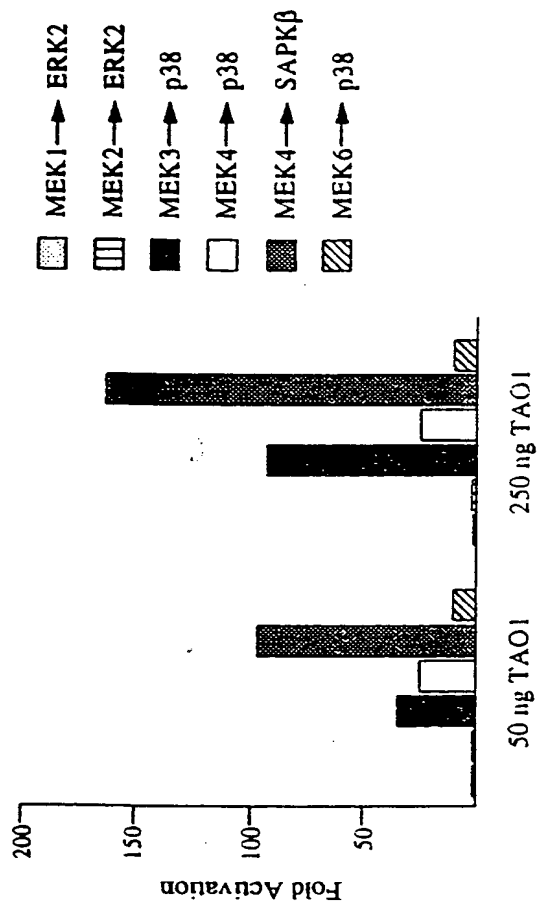


FIG. 9



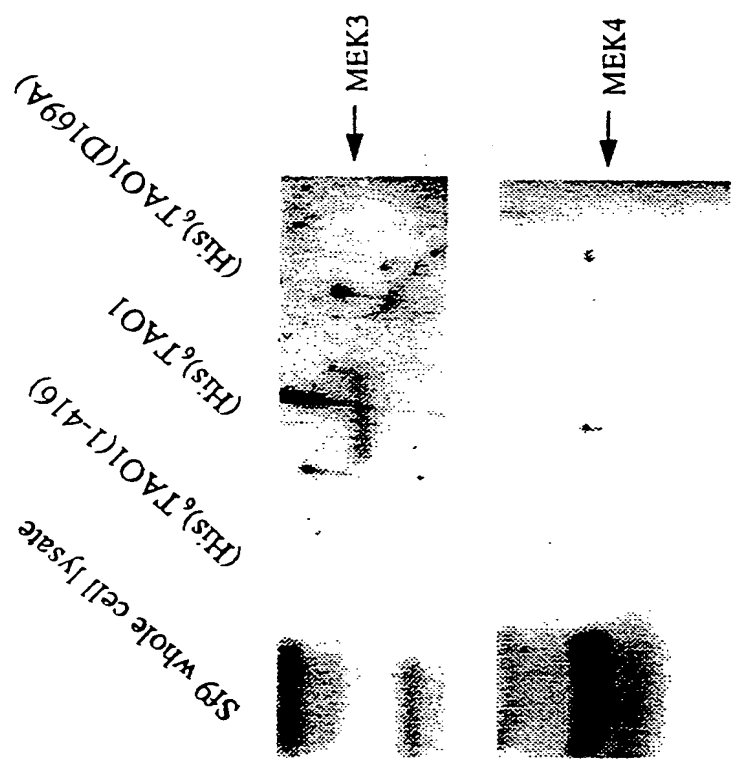


FIG. 11

```
Query:      2341 AGGAATCACCTACTGGAGACTACACCAAAGAGTGAGCACAAGCTGTTCTGAAAAGACTC 2400
             ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       12 ACGANTCACCAGTTTGAAGTTACTCCAAAGAATGAGCACAATAAATCTTAAAGACACTG 71

Query:     2401 AAGGAGGAACAGACTCGGAAGTTAGCCATCTTGGCTGAGCAGTATGATCATAGCATTAAT 2460
             ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       72 AAAGATGAGCAGACAAGAAAAC TTGCCATT TNGGCAGAGCAGTATGAACAGAGTATAAAT 131

Query:     2461 GAAATGCTCTCCACACAAGCTCTGCGTTTGGATGAAGCACAGGAAGCAGAATGCCAGGTT 2520
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       132 GAAATGATGGCCTCTCANGCGTTACGGCTAGATGAGGCTCAAGAAGCAGAATGCCAGGCC 191

Query:     2521 TTGAAGATGCAGCTACAGCAGGAACTGGAGCTGTTGAATGCATATCAGAGCAAAATCAAG 2580
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       192 TTGAGGCTACAGCTCCAGCAGGAAATGGAGCTGCTCAACGCCTACCAGAGCAAAATCAAG 251

Query:     2581 ATGCAGGCTGAGGCCCAACATGATCGAGAGCTTCGAGAGCTGGAACAAAGGGTCTCCCTT 2640
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       252 ATGCAACAGAGGCACAACATGAACGTGAGCTCCAGAAGCTAGAGCAGAGAGTGTCTCTG 311

Query:     2641 CGGAGAGCACTCTTAGAACAGAAGATTGAAGAAGAGATGTTGGCTTTGCAGAATGAACGC 2700
             ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       312 CGCAGAGCACACCTTGAGCAGAAGATTGAAGAGGAGCTGGCTGCCCTTCAGAAGGAACGC 371

Query:     2701 ACAGAACGAATACGTAGCCTGCTCGAGCGCCAGGCCAGAGAAATTGAAGCTTTTT 2754
             |   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:       372 AGCGAGAGAATAAAGAACCTATTGGAAAGGCAAGAGCGCAGAGATTGGAAACTTT 425
```

**FIG. 12**

Query: 964 GAACAAACATGTGCTTT AAAGTTCCTCTGATGTAGGGCGATCTTGAGGGATTTTCTGGA 905  
 Sbjct: 79 GAACAAAGTCATGCCTTAATAGTTCTGCTGATGTTGGCCTTTCCTGAGGTATTTTCTGCA 138  
 Query: 904 GGCAAGAATCTACAAAGTTTCGAAAATAATCAGACCATTTCATTAGACTGTAGTGTAGGGG 845  
 Sbjct: 139 AGCAGTAATCAACAAATCTCCTAAAGGAGTCTGTCCATTTCATTAGACTGTAACGTTGGGG 198  
 Query: 844 ATTCATTTTGGGCTATGTGATATAAGGCACTCATTGCATTTCATATTAAATAAGGAGGCT 785  
 Sbjct: 199 AGTCATTCTGGGCAATGTGATATAAGGCACTCATTGCATTTCATGTTGAAAAGGGGCGGCT 258  
 Query: 784 TCCTCTCGGCTAATTCAATACATGTTATTCCAAGAGACCATACATCAACTTTGCCATCAT 725  
 Sbjct: 259 TCCGTTCCGCCAATTCAATACAAGTGATGCCAAGTGACCAAATATCAACTTTCCCATCAT 318  
 Query: 724 ATTGTCCTTCATCCATGGCTAAAATTACTTCTGGGGCCATCCAATATGGTGTTCACAA 665  
 Sbjct: 319 ACTGTCCTTCATCCATAGCTAAGATCACCTCTGGAGCCATCCAGTAAGGTGTGCCACGA 378  
 Query: 664 AAGAATTGGCAGGG 651  
 Sbjct: 379 AGGAGTTGGCCAGG 392

FIG. 13

000101 94298960

```
Query:   2792 ACCATGTTACTAAACCTTAATCTCATGCTTTCAGAGTCAAAGCCTTCAATTTCCTCTGGCC 2733
          ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:    90 ACCAAATTCCCAAATCCCATCTCTGAGGCTCTCCATGTCAAAAGTTCAATCTCTCGCTCT 149

Query:   2732 TGGCGCTCGAGCAGGCTACGTATTCTGTTCTGTGCGTTCAATTCTGCAAAGCCAACATCTCT 2673
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   150 TGCCTTCCAATAGGTTCTTTATTCTCTCGCTGCGTTCTCTGAAGGGCAGCCAGCTCC 209

Query:   2672 TCTTTCAATCTTCTGTTCTAAGAGTGCTCTCCGAAGGGAGACCCTTTGTTCCAGCTCTCGA 2613
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   210 TCTTTCAATCTTCTGCTCAAGGTGTGGTCTGCGCAGAGACACTCTCTGCTCTAGCTTCTGG 269

Query:   2612 AGCTCTCGATCATGTTGGGCCCTCAGCCTGCATCTTGATTTTGCTCTGATATGCATTCAAC 2553
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   270 AGCTCACGTTCATGTTGTGCCTCTGTTNGNATCTTGATTTGNTCTGGTAGGCGTTGAGC 329

Query:   2552 AGCTCCAGTTCCTGCTGTAGCTGCATCTTCAAACCTGGCATTCTGCTTCCTGTGCTTCA 2493
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   330 AGCTCCATTTCTGCTGGAGCTGTAGCTCAAGGCCCTGGCATTCTGCTTCTTGAGCCTCA 389

Query:   2492 TCCAAACGCAGAGCTTGTGTGGAGAGCATTTCAATTAATGCTATGATCATACTGCTCAGCC 2433
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   390 TCTAGCCGTAACGCTTGAGAGGCCATCATTTCAATTTATACTCTGTTCACTAGCTCTGCC 449

Query:   2432 AAGATGGCTA 2423
          ||| ||||| |
Sbjct:   450 AAAATGGCAA 459
```

FIG. 14

[illegible]

```

Query: 2437 GAGCAGTATGATCATAGCATTAATGAAATGCTCTCCACACAAGCTCTGCGTTTGGATGAA 2496
          |||
Sbjct: 193 GAGCAGTATGAACAGAGTATAAATGAAATGATGGCCTCTCAAGCGTTACGGCTAGATGAG 252

Query: 2497 GCACA 2501
          |||
Sbjct: 253 GCTCA 257

```

*B*

**FIG. 15A and 15B**

```
Query:      2087 ATGAATCCATGCAAGAACTGGAGTTTCGCCACCTCAACACTATTTCAGAAGATGCGCTGTG   2146
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:       31 ACGAGTCCCCC GAGAGCTAGAGTACAGGCAGCTGCACACGTTACAGAAGCTACGCATGG   90

Query:     2147 AGTTGATCAGACTGCAACATCAAAC TGAGCTTACTAACCAGCTGGAATACAATAAGAGAA   2206
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      91 ATCTGATCCGTTTACAGCAC CAGACGGA ACTGGAAA ACCAGCTGGAGTACAATAAGAGGC   150

Query:     2207 GGGAACGGGAACTAAGACGGAAACATGTCATGGAAGTTTCGACAGCAGCCTAAGAGTTTGA   2266
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     151 GAGAAAGAGAACTGCACAGAAAGCATGTCATGGAACTTCGGCAACAGCCAAAAA ACTTAA   210

Query:     2267 AGTCTAAAGAACTCCAAATAAAAAAGCAGTTTT CAGGATA   2305
              ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:     211 AGGCCATGGAANTGCAATT TAAAAAACAGTTCCAGGAAA   249
```

FIG. 16



**A**

Query: 3228 GTGCATATGGTATATTTTATTCGTCTTTGTAAAGCGTTATGTTTTGTGTTTACTAATTGG 3287  
          |||||  
Sbjct: 31 GTGCATATGGTATATTTTATTCGTCTTTGTAAAGCGTTATGTTTTGTGTTTACTAATTGG 90  
Query: 3288 GATGTCATAGTATTTGGCTGCCGGG 3312  
          |||||  
Sbjct: 91 GATGTCATAGTACTTGGCTGCCGGG 115

**B**

Query: 3200 CTCACTTGGGTACTACCGGGTGAAGCTGTGCATATGGTATATTTT 3245  
          |||||  
Sbjct: 1 CTCACTTGGGTACTACAGTGTGAAGCTGAGTGCATATGGTATATT 46

**FIG. 17A and 17B**

09686346-101000



0968345 10100

```

Query:      187 GATCCGGAAAAAAGCTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCTTTGGAGCAGTT 246
             || || || || || || || || || || || || || || || || || || ||
Sbjct:      119 GACCCAGAGGAACTCTTCACCAAGCTTGACCGCATTGCCAAAGGCTCATTGGGGAGGTG 178
             || || || || || || || || || || || || || || || || || || ||
Query:      247 TATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAAT 296
             || || || || || || || || || || || || || || || || || || ||
Sbjct:      179 TACAAGGGGATCGACAACCACACCAAGGAAGTGGTGGCCATCAAGATCAT 228
             || || || || || || || || || || || || || || || || || || ||

```

***B***

**FIG. 19A and 19B**

```
Query:      866 TCATTAGACTGTAGTGTAGGGGATTCATTTTGGGCTATGTGATATAAGGCACCTCATTGCA 807
            ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     100 TCAGGATTCCTGGAGCTCTGGAGTTCATTAGTGGCTATCAGATACAATGCCCTGAGTGGA 159

Query:      806 TTCATATTAAATAAAGGAGGCTTCCTCTCGGCTAATTC AATACATGTTATTCCAAGAGAC 747
            || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     160 TTTTCATTAAGGTAAGGGGGTTCACCTTCCACCATTTC AATTGCCATAATTCCAAGAGAC 219

Query:      746 CATACATCAACTTT 733
            || | | | | | | | |
Sbjct:     220 CAGATATCAACTTT 233
```

**FIG. 20**